SUBJECT INDEX

A

Abelson murine leukemia virus
  immunoglobulin gene rearrangement and, 608
ACTH
  See Adrenocorticotrophic hormone
Acute myelogenous leukemia
  ETS2 oncogene and, 413-14
Additive gene action model, 342
Adenovirus E1A protein, 141-57
  cellular transcription factors and, 153-54
  function at promoter, 154-57
  structure and properties of, 143-45
  transcription activation of, 553-54
Adenovirus E1B-21kd polypeptide, 142
Adenovirus major late promoter, 145-47
Adenovirus major late transcription factor, 146-47
Adenovirus transcription
  E1A protein-mediated activation of
    mechanisms of, 153-57
    targets of, 145-53
Adenylate cyclase
  alcoholism and, 27-28
  Salmonella virulence and, 462
Adoption studies
  alcoholism and, 22-24
Adrenocorticotrophic hormone
  adrenal steroidogenesis and, 371
  alcoholism and, 28
Agrobacterium tumefaciens
  crown gall tumorigenesis and, 461-62
Alcohol
  metabolism of
    oxidative pathway for, 28-29
Alcohol abuse
  antisocial behavior disorder with, 23
Alcohol dehydrogenases
  alcohol metabolism and, 28
Alcoholism, 19-32
  adoption studies of, 22-24
  biochemical markers of, 27-29
  electrophysiological markers of, 26
  family studies of, 24-25
  male-limited, 23-24
  mapping to human genome, 29-32
  milieu-limited, 23-24
  personality and, 25
  twin studies of, 21-22
Aldehyde dehydrogenases
  alcohol metabolism and, 28
Aldosterone
  intravascular volume and blood pressure and, 372
Algae
  mating systems of
    sexual recognition processes in, 121-22
Alpha wave activity
  alcoholics and, 26
Alternative splicing, 527-66
  cis requirements in, 533-39
  developmental control and, 558-63
  evolution and, 563-66
  functional correlations of, 551-57
  mechanisms of, 542-51
  modes of, 531-33
  trans requirements in, 539-42
Alzheimer's disease
  chromosome 21 and, 410-13
Amino acid metabolism
  Rhizobium, 487-90
Androgens
  effects of, 372-73
Androstenedione
  effects of, 372-73
Anemia
  Fanconi
    homologous recombination and, 213
Antibodies
  diversity of
    molecular basis of, 609
  See also Immunoglobulins
Antigenic variation
  bacterial virulence and, 456-61
Antigens
  HLA
    alcoholic end-organ disease and, 27
Antisocial behavior disorder
  with alcohol abuse, 23
Arabidopsis thaliana
  self-compatibility in, 136
Artificial selection
  quantitative variation and, 340
Arylsulfatase A
  alcoholism and, 28
Ascaris suum
  chromatin diminution in, 591-92
Ascomycetes
  mating systems of
    sexual recognition processes in, 121-22
Atavistic polydactyly, 10
Ataxia telangiectasia
  homologous recombination and, 213
Auxin
  biosynthetic precursors to amino acids as, 487-88
  habituation for, 395-404
Azorhizobium, 484, 486

B

Bacillus anthracis
  virulence determinants in, 472
Bacillus subtilis
  degradative exoenzymes in regulation of, 322
Bacillus thuringiensis
  spore toxins of, 472
Bacterial virulence, 455-73
  antigenic variation and, 456-61
  gene expression and, 461-69
Bacteriocins
  plasmid genes for, 60
Bacteriophage lambda
  cII protein and, 188-90
  growth in *Escherichia coli lon* mutants, 173-74
  lysogenic state of
    cI gene product and, 402
  protein turnover in, 165
  tripartite operators in, 234-37
Barnase
  destabilization in, 298
  electrostatic interactions in, 301
Biogeography
  historical
    Drosophila melanogaster and, 426-28
Biological markers
  alcoholism and, 26-29
Biometric analysis
  quantitative variation and, 340
Blood groups
  MNS
    alcoholism and, 30

Blood pressure
mineralocorticoids and, 372
Bloom's syndrome, 213
B-lymphocyte differentiation
immunoglobulin chain expression in, 620
B lymphocytes
heavy-chain isotypes of, 628-29
Bordetella parapertussis, 465
Bordetella pertussis
antigenic modulation and variation in, 463-65
Borrelia hermsii
variable major proteins of, 461
Bottlenecks
population
additive variance and, 343
Bovine leukemia virus
DNA sequences of
integration of, 649
Bovine leukemia virus p34 protein, 142
Bovine pancreatic trypsin inhibitor
stability of
surface salt bridges and, 301
Bradyrhizobium, 484, 488
Bradyrhizobium japonicum
NifA proteins of
deletion analysis of, 326
Brain wave activity
alcoholics and, 26
Brassica
allelic specificity in, 130-31
S-alleles of
origin of, 134-36
self-compatibility in
origin of, 136
self-incompatibility in
molecular analysis of, 127-34
S-locus of
molecular organization of, 133
S-locus specific glycoproteins of
cell-type specificity of, 128-29
immunolocalization in stigma, 129-30
oligosaccharide chains of, 130-31
polypeptide moiety of, 131
S-multigene family of, 131-34
expressed members of, 133-34
Breast cancer
estrogen-induced gene in
mapped to chromosome 21, 413
Breeding values
distribution of
selection and, 350-51
Briquet's syndrome, 24
Brucella
virulence of, 473
Bussey Institute, 3-12

C

Caenorhabditis elegans
muscle development in, 507-22
Calcitonin/CGRP gene
processing in
regulation of, 546-47
Calcium phosphate/DNA
coprecipitation
extrachromosomal recombination and, 201
cAMP receptor protein
Salmonella virulence and, 462-63
Canavanine
heat-shock response and, 179-80
Carbohydrate metabolism
glucocorticoids and, 372
postnatal
cortisol deficiency and, 374
Cassette exons
alternative splicing and, 533
Cassette mutagenesis, 290-91, 303
Cell cycle
replication/condensation timing in
isochores and, 650-51
Cells
eukaryotic
ubiquitin in, 187
mammalian
recombination in, 199-220
nematode muscle
ultrastructure of, 509-13
plant
habituation of, 395-404
Characters
quantitative
Gaussian distribution of, 342
Chemical mutagens
Rhizobium and, 485-86
Chemoreceptors
signal transduction sensors and, 322
Chemotaxis
Rhizobium, 493-94
Cholera, 465
Cholesterol
conversion to cortisol, 371
Chromatin loops
isochores and, 648
Chromatography
reassociation kinetics of DNA components and, 645-46
Chromomeres
isochores and, 648
Chromosomal recombination, 206-13
Chromosome bands
isochores and, 646-48
Chromosomes
eukaryotic/prokaryotic, 58-59
polytene
telomeres and, 580
subtelomeric regions of, 589-91
translocation breakpoints on, 650
Ciliated protozoa
telomere formation in, 592
Cirrhosis
alcoholic
HLA system and, 27
Citrobacter
Vi capsular antigen synthesis in
genetic instability and, 177
Clinal variation
Drosophila melanogaster and, 439-40
Co1E1 plasmid, 52
Cockayne syndrome
homologous recombination and, 213
Collagen type VI
mapped to chromosome 21, 413
Compositional mapping
human genome research and, 655-57
Congenital adrenal hyperplasia
C4 genes associated with
genetic alterations in, 381-82
clinical forms of, 374-76
gene conversion in, 380-81
gene deletion causing, 384
genetic lesions in
frequency of, 382-84
genetic mapping in, 378-80
incidence of, 372, 376
nonclassical, 375-76
physiology of, 373-74
point mutations in, 385-89
salt-wasting, 375
southern blotting studies in, 378-84
virilizing, 375
Constitutive splicing
alternative splicing and, 545-66
mechanisms of, 529-31
Cortisol
alcoholism and, 28

carbohydrate metabolism and, 372
cholesterol conversion to, 371
Cortisol deficiency
prenatal manifestations of, 374
Corynebacterium diphtheriae
toxin gene expression in iron regulation of, 468
Covariance
genetic, 344-45
multivariate selection response and, 346-47
Cross-fostering, 346
Crown gall tumorigenesis
Agrobacterium tumefaciens and, 461-62
Crucifers
self-compatibility in, 136
self-incompatibility in
genetic and cellular basis of, 125-27
α-Crystallin
mapped to chromosome 21, 413
Cytochrome P450c21
steroid 21-hydroxylation and, 373
Cytochrome P450c21B gene
point mutations in, 385-87
polymorphism in, 385
Cytochrome P450c21B mRNA
point mutations in, 388-89
Cytochrome P450c21 genes
mapping of, 378-80
Cytochrome P450IIE1
microsomal ethanol oxidizing system and, 29
Cytokinin
habituation for, 395-404
Cytomegalovirus immediate early proteins, 142

D

Decay-accelerating factor gene
alternative splicing and, 552
Deletion analysis, 291, 326
deo operon
tripartite operators in, 238-39
Deoxycorticosterone, 373
Dihydrofolate reductase
destabilizing mutations in, 301
Directional selection
genetic covariance and, 345
Disulfide bonds
destabilizing protein mutations and, 301
DNA
heteroduplex
intrachromosomal recombination and, 213
microinjection of
extrachromosomal recombination and, 201
mitochondrial
Drosophila melanogaster and, 431-33
transfected
extrachromosomal metabolism of, 206
DNA ligase I
Bloom's syndrome and, 213
DNA looping, 227-47
feasibility of, 239-42
periodicity of, 240-42
positive control elements in, 245
regulatory systems with, 229-39
thermodynamics of, 239-40
DNA sequences
integration of
isochores and, 649-50
DNA sequence variation
Drosophila melanogaster and, 434-35
DNA termini
replication of
solutions for, 586-89
Dominance
pleiotropic loci and, 343-44
Down syndrome
chromosome 21 and, 409-14
Drosophila
gene transcription in
repression of, 580-81
P elements of
transposition of, 553
telomere-associated sequences in, 590-91
Drosophila ananassae
X chromosome of
restriction map surveys of, 278
Drosophila erecta, 426-48
Drosophila genes
alternative splicing and, 558-61
Drosophila mauritiana, 426-48
Drosophila melanogaster, 425-48
Adh activity in
variation in, 341
alternative alleles at complex loci in
pleiotropic effects of, 343
bristle number of
third chromosome and, 341
clinal variation in, 439-40
dessication tolerance in
selection for, 347
D/H ratio and, 440-41
DNA sequence variation in, 434-35
electrophoretic protein variation in, 430-31
ethanol tolerance in
selection response for, 342, 345
families of elements in, 259
gene-enzyme variation in, 428-30
gene-regulation variation in, 433-34
historical biogeography of, 426-28
life-cycle stages of
genetic variation and, 436-37
mitochondrial DNA variation in, 431-33
P element insertions in
detrimental mutations and, 259
phylogenetic relationships of, 444-45
populations of
genetic structure of, 438-39
quantitative variation in, 435-36
rDNA, 87-114
structure and genetics of, 89-90
rDNA magnification, 90-109
bobbed phenotype and, 102-5
control of, 107-8
genetic assays for, 91-94
mechanisms of, 97-102
mutants affecting, 105-6
pseudo-reversion mimicking, 94-95
significance of, 108-9
stability and heritability of, 95-96
rDNA recombination
interchromosomal, 109-12
Rex mutation and, 112-13
rDNA reduction, 96-97
sibling species of
genetic structure of, 437-38
species divergence in
evolutionary constraints on, 442-44
levels and patterns of, 441-42
theories of speciation and, 445-46
variation for wing length in
temperature and, 345
viability in
additive variance in, 354
Drosophila orena, 426-48
Drosophila pseudoobscura
restriction-map variation in, 278
Drosophila sechellia, 426-48

Drosophila simulans, 426-48
  nucleotide variation in, 342
  restriction map surveys of, 280
  variation for wing length in temperature and, 345
Drosophila teissieri, 426-48
Drosophila transposable elements
  accumulation in regions of restricted crossing over, 271-74
  distribution between homologous chromosomes, 266-67
  distribution between nonhomologous chromosomes, 267
  frequencies at individual chromosomal sites, 268-70
  linkage disequilibrium and, 270-71
  rates of movements of, 253-56
  restriction map surveys of, 274-80
  in situ hybridization and, 265-74
  structure and properties of, 252-53
Drosophila yakuba, 426-48

E

E1A protein, 141-57
  cellular transcription factors and, 153-54
  function at promoter, 154-57
  structure and properties of, 143-45
  transcription activation of, 553-54
Electroencephalogram
  alcoholics and, 26
Electron microscopy
  gal operon and, 231-32
Electroporation
  extrachromosomal recombination and, 201
Electrostatic interactions
  protein structure and, 300-1
Embryonic stem cells
  gene targeting in, 215-18
β-Endorphin
  alcoholism and, 28
Enhancers
  transcription initiation in eukaryotes and, 246
Enterobacteriaceae
  sulA analogs in, 177
Environment
  quantitative traits and, 345-46
Epigenetic change
  habituation and, 397-98
Epinephrine
  alcoholism and, 28
Epistasis, 343, 349
Epstein-Barr virus BMLF1 protein, 142
Epstein-Barr virus BRLF1 protein, 142
Epstein-Barr virus BZLF1 protein, 142
Erwinia stewartii
  RcsA analogs in, 172
Escherichia coli
  alanine-tRNA synthetase of
    deletion analysis of, 291
  arabinose operon of
    regulation of, 467
  aromatic amino acid biosynthesis in, 326
  ATP-binding proteins of, 460
  capR mutants of
    capsular polysaccharide synthesis and, 170-73
  Clp protease of, 183-85
    regulation of, 185
    substrates for, 184-85
  deo operon of
    tripartite operators in, 238-39
  energy-dependent proteases of
    substrate recognition by, 186-88
  enterotoxinogenic
    AraC similarity in, 467
  gal operon of
    bipartite operators in, 229-32
  lac operon of
    pseudomutation of, 402
    pseudo-operators in, 237-38
  Lon action in
    mechanism of, 178-79
  lon mutants of
    abnormal proteins and, 174-75
    lambda growth in, 173-74
    ultraviolet sensitivity of, 168-70
  Lon substrates in
    conservation of, 177-78
  Lon synthesis in
    heat-shock regulation of, 175-76
    phage T4 and, 176
  minichromosomes of
    replication of, 59
  proteolysis in, 163-91
    Alp-dependent, 185-86
    energy-independent, 188-91
    heat-shock response and, 179-83
    proteases and, 164-65
    RecA-dependent, 166-67
    substrates for, 165-66
  toxin gene expression in
    iron regulation of, 468
  tripartite *ara* operators in, 232-34
  type 1 pilus production in, 456-58
Esterase D
  alcoholism and, 30
Ethanol
  See Alcohol
Ethylene
  biosynthetic precursors to amino acids as, 487-88
Eukaryotes
  replicons of, 58-59
  telomeres of
    cloning and sequencing of, 583-85
  transcription initiation in
    distant DNA elements and, 246
Eukaryotic cells
  ubiquitin in
    functions of, 187
Evoked potential
  P300 amplitude of
    alcoholics and, 26
Evolution
  alternative splicing and, 563-66
  human genome
    isochores and, 652-53
  phenotypic
    neutral, 341-42
  polygenic
    number of loci and, 340
Evolutionary quantitative genetics, 337-62
Exons
  alternative splicing and, 533, 536
Exopolysaccharides
  Rhizobium, 492-93
Extrachromosomal recombination, 200-6
  double-strand breaks and, 204-5
  homology requirements of, 203-4
  single-stranded substrates for, 205
  timing of, 202-3
  types of, 202

F

Family studies
  alcoholism and, 24-25
Fanconi anemia
  homologous recombination and, 213

Fast muscle tyroponin-T
cassette exons of
alternative splicing of, 554
Fertility
21-hydroxylase deficiency
and, 375
Fetus
steroid 21-hydroxylation in,
373
Fibronectin
EDIIIA exon of
splicing of, 548
Fitness
estimation of, 359-61
heritability and, 346
phenotype and, 338, 357
Founder event, 343
F plasmid, 47-49
stability of, 60
Fungi
targeted recombination in,
214

G

gal operon
bipartite operators in, 229-32
Gametophytes
pollen inhibition in, 125
Gelsolin
localization of
alternative splicing and,
553
Gene conversion
congenital adrenal hyperplasia
and, 380-81
intrachromosomal, 210-11
Gene expression
alternative splicing in, 527-66
cis requirements in, 533-39
developmental control and,
558-63
evolution and, 563-66
functional correlations of,
551-57
mechanisms of, 542-51
modes of, 531-33
trans requirements in, 539-
42
bacterial virulence and, 461-
69
immunoglobulin, 609-13
Gene mapping
alcoholism and, 29-32
Genes
cloned
random mutagenesis of,
290-91
human
genomic distribution of,
651-52
isochores and, 641-44
Gene targeting, 214-18
Genetic analysis
self-incompatibility in plants
and, 127-28
Genetic covariance, 344-45
multivariate selection response
and, 346-47
Genetic mapping
cytochrome P450c21 genes
and, 378-80
human chromosome 21 and,
414-18
Genetic markers
alcoholism and, 26-29
Genetics
physiological
concepts of, 11-12
Genetic variation
Drosophila melanogaster and,
428-41
Genotype
phenotype and, 342
β-1,2-Glucans
Rhizobium, 493
Glucocorticoids
carbohydrate metabolism and,
372
Glutamine synthetase
ammonia assimilation in *Rhi-
zobium* and, 488
Glycine substitution
protein stability and, 299-300
Glycoproteins
S-locus specific
cell-type specificity of,
128-29
immunolocalization in stig-
ma, 129-30
oligosaccharide chains of,
130-31
polypeptide moiety of, 131
Gonococcal P.II protein
variation in, 459-60
Gonococcal pilins
phase and antigenic variation
in, 458-59
Gram-negative bacteria
Lon substrates in
conservation of, 177-78
Grasses
pollen inhibition in, 125
Guinea pigs
coat-color inheritance in, 4-6
inbred
decline in vigor among, 8-9
developmental anomalies
among, 10-11
differentiation among, 9-10

H

Habituation, 395-404
cellular basis for, 401-3
regulation of, 398-401
Haemophilus influenzae
capsule synthesis in
genetic instability and, 177
type b capsule expression in,
460-61
Harvard Institute
Bussey Institute, 3-12
Heat-shock proteases
protein degradation by, 181-
82
Heat-shock response
proteolysis in *Escherichia coli*
and, 179-83
Hepatitis B virus
DNA sequences of
integration of, 649
Hepatitis B virus X protein, 142
Heritability
environment and, 345-46
fitness and, 346
overdominance and, 356-57
Herpes simplex virus α-TIF pro-
tein, 142
Herpes simplex virus ICP27
protein, 142
Herpes simplex virus ICP4 pro-
tein, 142
Herpes simplex virus ICPO pro-
tein, 142
Heteroduplex DNA
intrachromosomal recombina-
tion and, 213
Hirsutism
21-hydroxylase deficiency
and, 375
Historical biogeography
Drosophila melanogaster and,
426-28
hnRNP proteins
alternative splicing and, 541
Human chromosome 21, 409-18
alphoid sequences on, 410-11
compositional mapping and,
656
genes encoded by
isolation of, 417-18
irradiation hybrids and, 416-
17
linkage map of, 416
long-range restriction digests
and, 417
physical map of, 414-15
ribosomal sequences on, 410
sequence of, 417
Human chromosome 21p
repeated sequences on, 410-
12
Human chromosome 21q
single-copy and repeated
sequences on, 412-14
Human genome
compositional mapping and,
655-57

isochore organization of, 637-57
mapping alcoholism to, 29-32
Human retrovirus tat proteins, 142
Hybrid dysgenesis, 254, 263
Hydrogen bonds
protein structure and, 300-1
Hydrophobic effect
stability of folded proteins and, 298
Hydroxyapatite chromatography
reassociation kinetics of DNA components and, 645-46
21-Hydroxylase
biology of, 372-73
21-Hydroxylase deficiency, 371-89
clinical forms of, 374-76
incidence of, 376
major histocompatibility complex and, 376-77
phenotypic manifestations of, 373-76
physiology of, 373-74
21-Hydroxylase genes, 377-78
21-Hydroxylase locus
genetics of, 376-78
17-Hydroxyprogesterone
21-hydroxylation of, 373

I

Iberis
self-incompatibility in, 125
Immunoglobulin gene rearrangement, 605-30
model systems for, 608-9
Immunoglobulin genes
assembled and incompletely assembled
expression of, 512-13
heavy-chain class switching in, 624-29
control of, 627-28
directed, 625-26, 628
mechanism of, 624-25
intragenic duplications in, 563
organization and expression of, 609-13
V(D)J recombination in, 613-15
recognition sequence requirements for, 616
recombinase components in, 618
scid mutation and, 617-18
variable region assembly of
control of, 619-24
mechanism of, 613-18
Immunoglobulins
diversity of
molecular basis of, 609
Inbreeding, 4
brother-sister inbred lines and, 8-9
developmental anomalies and, 10-11
Influenza virus
RNA splicing in, 548
In situ hybridization
Drosophila transposable elements and, 265-74
Interchromosomal recombination, 206-7
Interphase nucleus
telomeres and, 580
Intrachromosomal recombination, 207-8
accuracy of, 212
heteroduplex DNA and, 213
homology requirements of, 211-12
rates of, 208-9
reciprocal, 209
Intron binding protein
alternative splicing and, 541
Introns
alternative splicing and, 532, 536
Ionizing radiation
intrachromosomal recombination and, 213
Iron
bacterial virulence and, 468-69
Isochores, 638-41
cell cycle and, 650-51
chromosome bands and, 646-48
CpG doublets and islands and, 644, 652
genes and, 641-44
genome evolution and, 652-53
genomic distribution of genes and, 651-52
integration of DNA sequences and, 649-50
long-range physical mapping and, 649
"single-copy" and middle-repetitive sequences and, 645-46
translocation breakpoints and, 650

K

Kanamycin nucleotidyltransferase
enhanced stability mutations in, 304
Klebsiella
RcsA analogs in, 172
Klebsiella pneumoniae
NifA proteins of
deletion analysis of, 326

L

lac operon
pseudomutation of, 402
pseudo-operators in, 237-38
lac repressor gene
codon positions in suppressed nonsense mutations at, 296-97
Lactoferrin
bacterial virulence and, 468
Lambda Cro
destabilizing mutations in, 300-1
genes encoding
missense mutations and, 294-96
Lambda O protein
proteolysis and, 166
Lambda repressor
destabilization in, 298
destabilizing mutations in, 300-1
genes encoding
missense mutations and, 294-95
Legionella
virulence of, 473
Leukemia
acute myelogenous
ETS2 oncogene and, 413-14
Leukocyte adhesion deficiency disease
CD18 gene and, 414
Leukocyte adhesion molecule-1
mapped to chromosome 21, 413
Lipopolysaccharides
Rhizobium, 493
Listeria
virulence of, 473
Lysozyme
destabilization in, 298

M

Macroevolution, 338
application of models to, 359-61
Maize
transposable elements of, 71-82
biological relevance of, 80-82
gene expression and, 403
Major histocompatibility complex

21-hydroxylase deficiency
and, 376-77
Mammalian cells
recombination in, 199-220
chromosomal, 206-13
extrachromosomal, 200-6
Mammals
coat-color inheritance in, 4-6
gametic recognition in, 122
immunoglobulin gene
rearrangement in, 605-30
telomeres of
cloning and sequencing of, 583-85
Melanin
synthesis of
Rhizobium and, 489
Menstruation
21-hydroxylase deficiency and, 375
Microevolution, 338
application of models to, 359-61
Microsomal ethanol oxidizing system, 29
Mineralocorticoids
intravascular volume and blood pressure and, 372
Missense mutations
protein stability and, 294-96
Mitochondrial DNA
Drosophila melanogaster and, 431-33
Mitomycin C
intrachromosomal recombination and, 213
MNS blood group
alcoholism and, 30
Monoamine oxidase
platelet
alcoholism and, 27
Morphological traits
heritable variation for, 351-57
Mouse mammary tumor virus
DNA sequences of, 649
Mouse mammary tumor virus 3' orf polypeptide, 142
Muller's ratchet, 264-65, 273-74
Mutagenesis
cassette, 290-91, 303
Mutations
habituation and, 397-98
missense
protein stability and, 294-96
nonsense
lac repressor gene and, 296-97
point
congenital adrenal hyperplasia and, 385-89
Mutation-selection balance, 352-53
polygenic, 341-42
Mu transposase
proteolysis and, 166
Mycobacterium
virulence of, 473
Myofilament proteins
nematode muscle and, 513-18
Myosin heavy chains
nematode muscle and, 513-16

N

Natural selection
abundance of elements within populations and, 258-59
environmental extremes and, 345
Neisseria gonorrhoeae
virulence of, 458-60
Nematode muscle, 507-22
cells of
ultrastructure of, 509-13
genetic analysis of, 518-19
protein components of, 513-18
thick filament assembly in, 520-21
Neogenome, 653-55
Neural cell adhesion molecules
alternative splicing and, 551-52
Nicotiana
pollen inhibition in, 125
Nitrogenase enzyme
Rhizobium and, 489
Nitrogen fixation, 483
Nonsense mutations
lac repressor gene and, 296-97
NR1 plasmid, 50-52
Nucleases
intrachromosomal recombination and, 213
Nucleosomes
isochores and, 648

O

Ompt product, 191
Oncogene *ETS2*
mapped to chromosome 21, 413
Otocephaly, 12
Overdominance
heritability and, 356-57
polymorphism and, 354
Oxytricha
telomeres of
sequencing of, 582-86
formation of, 593-94

P

P1 plasmid, 49-50
Paleogenome, 653-55
Pancreatitis
alcoholic
HLA system and, 27
Papillomavirus E7 protein, 142
Papilloma virus full-length E2 protein, 142
Paramecium
telomere formation in, 592
Paramyosin
nematode muscle and, 513-16
Parascaris equorum
chromatin diminution in, 591-92
Pedigree analysis
alcoholism and, 30
Peptide hormones
generation of
alternative splicing and, 557
Personality
alcoholism and, 25
Pertussis, 463
Phage T4
Escherichia coli Lon synthesis and, 176
Phage T4 lysozyme
conformational changes in, 302
destabilizing mutations in, 300-1
electrostatic interactions in, 301
genes encoding
missense mutations and, 294-95
Phenotype
fitness and, 338, 357
genotype and, 342
Phenotypic evolution
neutral, 341-42
Phenotypic variability
alternative splicing and, 564
Phosphofructokinase liver type
mapped to chromosome 21, 413
Phospholipase D
alcoholism and, 28
Phosphorylation
E1A protein and, 144
Physiological genetics
concepts of, 11-12
Planaria
development and differentiation in
physiological gradients controlling, 12
Plant cells
cultured
habituation of, 395-404

Plant hormones
biosynthetic precursors to amino acids as, 487-88
Plants
self-compatibility in origin of, 136
self-incompatibility in diversity of, 122-25
molecular analysis of, 127-34
sporophytic control of, 125-27
telomeres of
cloning and sequencing of, 583-85
Plant tumorigenesis, 400-1
Plasmids, 37-65
anticlumping systems of, 43
equipartition in, 56-57, 64-65
examples of, 46-52
killer systems of, 43-44
maintenance of
strategies for, 59-62
partition in
host chromosome and, 58
host structures in, 57-58
loci for, 52-53
models for, 54-56
one-pair, 56-57, 64-65
randomization during, 53-54
partition-partition incompatibility in
randomization during, 62-64
Rhizobium, 486
site-specific recombination systems of, 41-43
stable inheritance of, 38-39
identification of systems for, 45-46
true partition systems of, 44-45
Plasmodium
telomere-associated sequences in, 591
Platelet-derived growth factor gene
alternative splicing and, 552-53
Platelet monoamine oxidase
alcoholism and, 27
Pleiotropy, 343, 355-57
Point mutations
congenital adrenal hyperplasia and, 385-89
Polydactyly
atavistic, 10
single-gene-induced, 12
Polygenes, 341-42
Polygenic evolution
number of loci and, 340
Polygenic mutation-selection balance, 341-42
Polymerase chain reaction
gene targeting and, 218
Polymerases
intrachromosomal recombination and, 213
Polymorphism
overdominance and, 354
Polyoma virus large-T antigen, 142
Polypyrimidine tract
alternative splicing and, 534-35
Polytene chromosomes
telomeres and, 580
Population bottlenecks
additive variance and, 343
Pregnancy
steroid 21-hydroxylation during, 373
Progesterone
21-hydroxylation of, 373
Prokaryotes
replicons of, 58-59
signal-transducing regulatory pairs in, 311-30
CheA/CheY + CheB, 318-10
CheB subclass, 327-28
CheY subclass, 328
conserved interaction between, 317-21
cross-talk and, 320-21
EnvZ/OmpR, 319-20
function of regulator in, 324-28
function of sensor in, 321-24
genetic analysis of, 328-29
homology between, 316-17
NtrB/NtrC, 317-18
NtrC subclass, 325-27
OmpR subclass, 327
PhoR/PhoB, 320
transposition in
regulation of rate of, 256
Prolactin
alcoholism and, 28
Proline substitution
protein stability and, 299-300
Proopiomelanocortin
synthesis of
plasma cortisol levels and, 371
Proteases
energy-dependent
substrate recognition by, 186-88
heat-shock
protein degradation by, 181-82
proteolysis in *Escherichia coli* and, 164-65
Protein kinase A
adenovirus transcription and, 151
Protein polymorphism
Adh activity in *Drosophila melanogaster* and, 341
Proteins
function of
residues important for, 302-4
hydrophobic core of
substitutions affecting, 297-99
interactions with telomeres, 594-97
localization of
alternative RNA processing and, 551-53
morphogenetic
alternative splicing of, 561-63
mutant
conformational changes in, 302
proteolytic sensitivity of, 304-5
mutations causing reduction or loss of activity, 294-96
stability of
glycine and proline substitutions and, 299-300
measurement of, 293
mutations enhancing, 304
neutral mutations and, 296-97
structures of
electrostatic interactions and, 300-1
folded and unfolded, 291-93
hydrogen bonds and, 300-1
TATA-binding
E1A protein and, 145-46
telomere replication and, 588
viral transactivating, 141-43
Proteolysis
Escherichia coli, 163-91
Alp-dependent, 185-86
energy-independent, 188-91
heat-shock response and, 179-83
proteases and, 164-65
RecA-dependent, 166-67
substrates for, 165-66
Protoplast fusion
extrachromosomal recombination and, 201
Protozoa
ciliated
telomere formation in, 592

pSC101 plasmid, 52
Pseudomonas
alginate synthesis in
genetic instability and, 177
Pseudomonas aeruginosa
exotoxin A gene of
regulation of, 469
signal-transducing regulatory pairs in, 317
Pseudomonas atlantica
exopolysaccharide synthesis in genetic instability and, 177
Pseudomonas syringae pv. *phaseolicola*
HrpS regulatory protein in NtrC class in, 326
Pseudorabies virus immediate early protein, 142, 146
Purine
Rhizobium symbiosis and, 488-89
Purine de novo biosynthetic pathway
chromosome 21 and, 413
Pyrimidine
Rhizobium symbiosis and, 488-89
Pyruvate kinase
isoforms of
alternative splicing of, 554-55

Q

Quantitative characters
Gaussian distribution of, 342
Quantitative traits
Drosophila melanogaster and, 435-36
environment and, 345-46
loci affecting
markers identifying, 341
Quantitative variation, 337-62
genetics of, 339-44
number of loci and, 339-41
patterns of, 344-47
selection and, 347-51

R

R1 plasmid, 50-52
stability of, 60
Radiation
ionizing
intrachromosomal recombination and, 213
Random drift, 343
Raphanus
self-incompatibility in, 125
S-genotypes of, 134-35
rDNA
structure and genetics of, 89-90
rDNA magnification, 90-109
bobbed phenotype and, 102-5
control of
model for, 107-8
genetic assays for, 91-94
mechanisms of, 96-102
mutants affecting, 105-6
pseudo-reversion mimicking, 94-95
significance of, 108-9
stability and heritability of, 95-96
rDNA recombination
interchromosomal, 109-12
Rex mutation and, 112-14
Recombination
chromosomal, 206-13
extrachromosomal, 200-6
double-strand breaks and, 204-5
homology requirements of, 203-4
single-stranded substrates for, 205
timing of, 202-3
types of, 202
interchromosomal, 206-7
intrachromosomal, 207-8
accuracy of, 212
heteroduplex DNA and, 213
homology requirements of, 211-12
rates of, 208-9
reciprocal, 209
targeted, 214-18
Recombination enzymes
intrachromosomal recombination and, 213
Relapsing fever, 461
Replicons
eukaryotic/prokaryotic, 58-59
"ideal" basic
characteristics of, 39-40
random distribution of
helper elements aiding, 41-43
Restriction-enzyme analysis
nucleotide variation in *Drosophila simulans* and, 342
Restriction mapping
Drosophila transposable elements and, 274-80
Retrotransposons, 72
Rhizobium, 483-98
behavior and classification of, 484
cell surface components of, 492-94
as genetic system, 484-87
metabolic genes of, 487-90
nif, *fix* and *dct* genes of, 494-97
nodulation genes of, 490-92
Rhizobium leguminosarum
DctD regulator in, 326
Rhizobium meliloti
NifA proteins of
deletion analysis of, 326
Rhodopseudomonas capsulata
signal-transducing regulatory pairs in, 317
RNA polymerase
transcription initiation by
negative control of, 24245
regulatory proteins and, 228
RNA polymerase III
adenovirus transcription and, 152
RNA splicing
See Alternative splicing
Rous sarcoma virus
DNA sequences of
integration of, 649
RNA splicing in, 548

S

Saccharomyces
gene transcription in
repression of, 580-81
telomere-associated sequences in, 589-91
Saccharomyces cerevisiae
transcriptional regulatory proteins of
deletion analysis of, 291
S-alleles
origin of, 134-36
Salmonella
flagellins of
phase variation of, 470
virulence gene expression in
stage-specific, 472
virulence of
regulation of, 462-63
Salmonella cholerasuis, 463
Salmonella typhimurium
arabinose operon of
regulation of, 467
ATP-binding proteins of, 460
Lon protease of, 178
signal-transducing regulatory pairs in, 317
virulence of
regulation of, 462-63
Salt bridges
protein structure and, 300-1
Salvia lyrata
leaf length and number in
plant spacings and, 345

Schizosaccharomyces pombe
telomeres of
sequence of, 585
Selection, 4
artificial
quantitative variation and, 340
directional, 339
genetic covariance and, 345
Drosophila melanogaster and, 437-41
limits to, 357-59
natural
abundance of elements within populations and, 258-59
environmental extremes and, 345
pleiotropy and, 343
quantitative variation and, 347-51
Selection response
long-term, 341-42
multivariate
genetic covariance and, 346-47
Self-compatibility
in plants
origin of, 136
Self-incompatibility
in plants
diversity of, 122-25
genetic and cellular basis of, 125-27
molecular analysis of, 127-34
sporophytic control of, 125-27
Shigella flexneri
virulence of
temperature control of, 468
Sigma 32
heat-shock response and, 179
proteolysis and, 180-81
Silencers
transcription initiation in eukaryotes and, 246
Sister chromatids
reciprocal intrachromosomal interactions in, 209
Slime molds
mating systems of
sexual recognition processes in, 121-22
S locus
molecular organization of, 133
S-locus specific glycoproteins
cell-type specificity of, 128-29
immunolocalization in stigma, 129-30
oligosaccharide chains of, 130-31
polypeptide moiety of, 131
S-multigene family, 131-34
expressed members of, 133-34
snRNA
alternative splicing and, 539-40
snRNP proteins
alternative splicing and, 540
Somatization disorder
high- and low-frequency alcoholic families and, 24
SOS response, 166, 168
Southern blotting analysis
congenital adrenal hyperplasia and, 378-84
Species divergence
Drosophila melanogaster and, 441-44
Spliceosomes
alternative splicing and, 541-42
Sporophytes
pollen inhibition in, 125
self-incompatibility in plants and, 125-27
Staphylococcal nuclease
conformational changes in, 302
destabilizing mutations in, 300-1
enhanced stability mutations in, 304
genes encoding
missense mutations in, 294-95
Staphylococcus
plasmid pT181 of, 52
Staphylococcus aureus
protoplasts of
plasmid loss and, 57-58
Stem cells
embryonic
gene targeting in, 215-18
Steroidogenic pathway, 371
Streptococcal M proteins, 461
Stylonchia
telomeres of
sequencing of, 582
Subtilisin
enhanced stability mutations in, 304
Superoxide dismutase-1
mapped to chromosome 21q22, 413
SV40 large-T angiten, 142
SV40 small-t antigen, 142

T

Targeted recombination, 214-18
TATA-binding proteins
E1A protein and, 145-46
T-cell receptor gene
intragenic duplications in, 563
Telomerase, 588-89, 594-95
Telomeres, 579-98
formation of, 591-94
function of, 580-81
importance of, 597-98
proteins interacting with, 594-97
replication of, 586-89
sequence and structure of, 581-86
Testosterone
effects of, 372-73
genital differentiation and, 374
Tetrahymena
telomere formation in, 592-94
Tetrahymena thermophila
telomeres of
sequencing of, 581-86
Tn903 transposase
proteolysis and, 165
Tobacco
transgenic
deletion derivatives of *Ac* in, 75-76
Topoisomerase II
chromatin loops and, 648
Traits
continuous
spatial variation in, 355
morphological
heritable variation for, 351-57
quantitative
Drosophila melanogaster and, 435-36
environment and, 345-46
markers identifying, 341
Transferrin
bacterial virulence and, 468
Transgenic mice
immunoglobulin gene rearrangement and, 609
Transposable elements
DNA-sequence similarity among, 265
Drosophila
accumulation in regions of crossing over, 271-74
distribution between homologous chromosomes, 266-67
distribution between nonhomologous chromosomes, 267
frequencies at individual chromosomal sites, 268-70
linkage disequilibrium and, 270-71
rates of movements of, 253-56

restriction map surveys of, 274-80
structure and properties of, 252-53
dynamics in finite populations, 262-65
dynamics in infinite populations, 257-62
frequencies of
probability distribution of, 262-63
insertion-deletion variation and, 342
maize, 71-82
biological relevance of, 80-82
gene expression and, 403
natural selection and, 258-59
population models of, 256-65
stochastic loss of, 263-64
Transposases
proteolysis and, 165-66
Transposition
En/Spm
regulation of, 78-80
En/Spm and *Ac* systems of
biochemical analysis of, 76-78
structural features of, 72-73
excision of parental elements and, 257-58
mechanism of, 72-78
models for, 73-74
prokaryotic
regulation of rate of, 256
rates of
evolution of, 260-62
substrates for, 75-76
specificity of, 74-75
Tropomyosin
nematode muscle and, 513-16
Troponins
nematode muscle and, 513-16
Trypanosoma
gene transcription in telomeres and, 581
Tryptophan biosynthesis
Rhizobium
pathway for, 488
Tumorigenesis
crown gall
Agrobacterium tumefaciens and, 461-62
plant, 400-1
Twin studies
alcoholism and, 21-22
Typhoid fever, 462
Tyrosinase
albino locus in guinea pigs and, 7
Tyrosine
as chromogen, 7

U

U2AF protein
alternative splicing and, 541
Ubiquitin
eukaryotic cells and, 187
Ultraviolet light
Escherichia coli lon mutations and, 168-70
intrachromosomal recombination and, 213
Ultraviolet mutagenesis
Rhizobium and, 485-86
University of Chicago
Zoology Department, 12-14

V

Variation
antigenic
bacterial virulence and, 456-61
genetic
Drosophila melanogaster and, 428-41
quantitative, 337-62
genetics of, 339-44
number of loci and, 339-41
patterns of, 344-47
selection and, 347-51
Varicella zoster virus 140kd protein, 142
Vibrio cholerae
membrane proteins in transcriptional activator for, 327
TCP pili genes of
regulation of, 471
virulence determinants in regulation of, 465-66
Viral DNA sequences
integration of
isochores and, 649-50
Viral transactivating proteins, 141-43
Virilism
21-hydroxylase deficiency and, 375
Virulence
bacterial, 455-73
antigenic variation and, 456-61
gene expression and, 461-69
Viruses
RNA splicing in, 548

W

Whooping cough, 463
Wright, Sewall, 1-16
Wright-Castle formula, 340

X

Xeroderma pigmentosum
homologous recombination and, 213

Y

Yeast
2-micron circle replicon of, 59
Yeast iso-1-cytochrome *c*
genes encoding
missense mutations and, 294-96
Yersinia enterocolitica
invasive properties of
temperature and, 472
low-calcium response of, 466-67
Yersinia pestis
low-calcium response of, 466-67
Yersinia pseudotuberculosis
low-calcium response of, 466-67